Genetic analysis reveals no common link in autism

The search for genes that contribute to the risk for autism has made tremendous strides over the past 3 years. As this field has advanced, investigators have wondered whether the diversity of clinical features across patients with autism reflects heterogeneous sources of genetic risk.

A large group of collaborating scientists used data from the Simons Simplex Collection, a project that extensively characterized 2576 autism simplex families, the largest such cohort amassed to date and for which the data is now available in a permanent repository.

The availability of this vast collection allowed the researchers to create phenotypic subgroups. In addition to the whole sample, this resulted in 11 subgroups of patients with similar diagnostic, IQ and symptom profiles. They then analyzed the genotypic data in an attempt to discover common genetic variants that confer risk for autism spectrum disorder.

Their results did not identify any genome-wide significant associations in the overall sample or in the phenotypic subgroups. This means that the extreme clinical variability observed among patients with autism spectrum disorder does not closely reflect common genetic variation.

The GLP aggregated and excerpted this blog/article to reflect the variety of news, opinion and analysis. Read full, original post: Is there such a thing as ‘pure’ autism? Genetic analysis says no